

SEQUENCE LISTING

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<120> METHODS FOR HIGH-TEMPERATURE HYDROLYSIS OF GALACTOSE-CONTAINING
OLIGOSACCHARIDES IN COMPLEX MIXTURES

<130> 9207.4

<150> US 60/220,211

<151> 2000-07-22

<160> 2

<170> PatentIn version 3.1

<210> 1

<211> 1659

<212> DNA

<213> Thermotoga maritima

<220>

<221> CDS

<222> (1)..(1659)

<223>

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 gag aaa aac ttc aca gtt gag ttc gcg gtg gag aag ata cac ctt ggc	96
Glu Lys Asn Phe Thr Val Glu Phe Ala Val Glu Lys Ile His Leu Gly	
20 25 30	
 tgg aag atc tcc ggc agg gtg aag gga agt ccg gga agg ctt gag gtt	144
Trp Lys Ile Ser Gly Arg Val Lys Gly Ser Pro Gly Arg Leu Glu Val	
35 40 45	
 ctt cga acg aaa gca ccg gaa aag gta ctt gtg aac aac tgg cag tcc	192
Leu Arg Thr Lys Ala Pro Lys Val Leu Val Asn Asn Trp Gln Ser	
50 55 60	
 tgg gga ccg tgc agg gtg gtc gat gcc ttt tct ttc aaa cca cct gaa	240
Trp Gly Pro Cys Arg Val Val Asp Ala Phe Ser Phe Lys Pro Pro Glu	
65 70 75 80	
 ata gat ccg aac tgg aga tac acc gct tcg gtg gtg ccc gat gta ctt	288
Ile Asp Pro Asn Trp Arg Tyr Thr Ala Ser Val Val Pro Asp Val Leu	
85 90 95	

gaa aga aaa aag aac ata aca cca att cag gcg ttc aga aaa ggg att	1056
Glu Arg Lys Lys Asn Ile Thr Pro Ile Gln Ala Phe Arg Lys Gly Ile	
340 345 350	
gag acg atc aga aaa gcg gtg gga gaa gat tct ttc atc ctc gga tgc	1104
Glu Thr Ile Arg Lys Ala Val Gly Glu Asp Ser Phe Ile Leu Gly Cys	
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ggc tct ccc ctt ctt ccc gca gtg gga tgc gtc gac ggg atg agg ata	1152
Gly Ser Pro Leu Leu Pro Ala Val Gly Cys Val Asp Gly Met Arg Ile	
370 375 380	
gga cct gac act gcg ccg ttc tgg gga gaa cat ata gaa gac aac gga	1200
Gly Pro Asp Thr Ala Pro Phe Trp Gly Glu His Ile Glu Asp Asn Gly	
385 390 395 400	
gct ccc gct gca aga tgg gcg ctg aga aac gcc ata acg agg tac ttc	1248
Ala Pro Ala Ala Arg Trp Ala Leu Arg Asn Ala Ile Thr Arg Tyr Phe	
405 410 415	
atg cac gac agg ttc tgg ctg aac gac ccc gac tgt ctg ata ctg aga	1296
Met His Asp Arg Phe Trp Leu Asn Asp Pro Asp Cys Leu Ile Leu Arg	
420 425 430	
gag gag aaa acg gat ctc aca cag aag gaa aag gag ctc tac tcg tac	1344
Glu Glu Lys Thr Asp Leu Thr Gln Lys Glu Lys Glu Leu Tyr Ser Tyr	
435 440 445	
acg tgt gga gtg ctc gac aac atg atc ata gaa agc gat gat ctc tcg	1392
Thr Cys Gly Val Leu Asp Asn Met Ile Ile Glu Ser Asp Asp Leu Ser	
450 455 460	
ctc gtc aga gat cat gga aaa aag gtt ctg aaa gaa acg ctc gaa ctc	1440
Leu Val Arg Asp His Gly Lys Lys Val Leu Lys Glu Thr Leu Glu Leu	
465 470 475 480	
ctc ggt gga aga cca cgg gtt caa aac atc atg tcg gag gat ctg aga	1488
Leu Gly Gly Arg Pro Arg Val Gln Asn Ile Met Ser Glu Asp Leu Arg	
485 490 495	
tac gag atc gtc tcg tct ggc act ctc tca gga aac gtc aag atc gtg	1536
Tyr Glu Ile Val Ser Ser Gly Thr Leu Ser Gly Asn Val Lys Ile Val	
500 505 510	
gtc gat ctg aac agc aga gag tac cac ctg gaa aaa gaa gga aag tcc	1584
Val Asp Leu Asn Ser Arg Glu Tyr His Leu Glu Lys Glu Gly Lys Ser	
515 520 525	
tcc ctg aaa aaa aga gtc gtc aaa aga gaa gac gga aga aac ttc tac	1632
Ser Leu Lys Lys Arg Val Val Lys Arg Glu Asp Gly Arg Asn Phe Tyr	
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Phe Tyr Glu Glu Gly Glu Arg Glu	
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 <212> PRT
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Trp	Lys	Ile	Ser	Gly	Arg	Val	Lys	Gly	Ser	Pro	Gly	Arg	Leu	Glu	Val	35	40	45	
Leu	Arg	Thr	Lys	Ala	Pro	Glu	Lys	Val	Leu	Val	Asn	Asn	Trp	Gln	Ser	50	55	60	
Trp	Gly	Pro	Cys	Arg	Val	Val	Asp	Ala	Phe	Ser	Phe	Lys	Pro	Pro	Glu	65	70	75	80
Ile	Asp	Pro	Asn	Trp	Arg	Tyr	Thr	Ala	Ser	Val	Val	Pro	Asp	Val	Leu	85	90	95	
Glu	Arg	Asn	Leu	Gln	Ser	Asp	Tyr	Phe	Val	Ala	Glu	Glu	Gly	Lys	Val	100	105	110	
Tyr	Gly	Phe	Leu	Ser	Ser	Lys	Ile	Ala	His	Pro	Phe	Phe	Ala	Val	Glu	115	120	125	
Asp	Gly	Glu	Leu	Val	Ala	Tyr	Leu	Glu	Tyr	Phe	Asp	Val	Glu	Phe	Asp	130	135	140	
Asp	Phe	Val	Pro	Leu	Glu	Pro	Leu	Val	Val	Leu	Glu	Asp	Pro	Asn	Thr	145	150	155	160
Pro	Leu	Leu	Leu	Glu	Lys	Tyr	Ala	Glu	Leu	Val	Gly	Met	Glu	Asn	Asn	165	170	175	
Ala	Arg	Val	Pro	Lys	His	Thr	Pro	Thr	Gly	Trp	Cys	Ser	Trp	Tyr	His	180	185	190	
Tyr	Phe	Leu	Asp	Leu	Thr	Trp	Glu	Glu	Thr	Leu	Lys	Asn	Leu	Lys	Leu	195	200	205	
Ala	Lys	Asn	Phe	Pro	Phe	Glu	Val	Phe	Gln	Ile	Asp	Asp	Ala	Tyr	Glu	210	215	220	
Lys	Asp	Ile	Gly	Asp	Trp	Leu	Val	Thr	Arg	Gly	Asp	Phe	Pro	Ser	Val	225	230	235	240
Glu	Glu	Met	Ala	Lys	Val	Ile	Ala	Glu	Asn	Gly	Phe	Ile	Pro	Gly	Ile	245	250	255	
Trp	Thr	Ala	Pro	Phe	Ser	Val	Ser	Glu	Thr	Ser	Asp	Val	Phe	Asn	Glu	260	265	270	

His Pro Asp Trp Val Val Lys Glu Asn Gly Glu Pro Lys Met Ala Tyr
 275 280 285
 Arg Asn Trp Asn Lys Lys Ile Tyr Ala Leu Asp Leu Ser Lys Asp Glu
 290 295 300
 Val Leu Asn Trp Leu Phe Asp Leu Phe Ser Ser Leu Arg Lys Met Gly
 305 310 315 320
 Tyr Arg Tyr Phe Lys Ile Asp Phe Leu Phe Ala Gly Ala Val Pro Gly
 325 330 335
 Glu Arg Lys Lys Asn Ile Thr Pro Ile Gln Ala Phe Arg Lys Gly Ile
 340 345 350
 Glu Thr Ile Arg Lys Ala Val Gly Glu Asp Ser Phe Ile Leu Gly Cys
 355 360 365
 Gly Ser Pro Leu Leu Pro Ala Val Gly Cys Val Asp Gly Met Arg Ile
 370 375 380
 Gly Pro Asp Thr Ala Pro Phe Trp Gly Glu His Ile Glu Asp Asn Gly
 385 390 395 400
 Ala Pro Ala Ala Arg Trp Ala Leu Arg Asn Ala Ile Thr Arg Tyr Phe
 405 410 415
 Met His Asp Arg Phe Trp Leu Asn Asp Pro Asp Cys Leu Ile Leu Arg
 420 425 430
 Glu Glu Lys Thr Asp Leu Thr Gln Lys Glu Lys Glu Leu Tyr Ser Tyr
 435 440 445
 Thr Cys Gly Val Leu Asp Asn Met Ile Ile Glu Ser Asp Asp Leu Ser
 450 455 460
 Leu Val Arg Asp His Gly Lys Lys Val Leu Lys Glu Thr Leu Glu Leu
 465 470 475 480
 Leu Gly Gly Arg Pro Arg Val Gln Asn Ile Met Ser Glu Asp Leu Arg
 485 490 495
 Tyr Glu Ile Val Ser Ser Gly Thr Leu Ser Gly Asn Val Lys Ile Val
 500 505 510
 Val Asp Leu Asn Ser Arg Glu Tyr His Leu Glu Lys Glu Gly Lys Ser
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 Ser Leu Lys Lys Arg Val Val Lys Arg Glu Asp Gly Arg Asn Phe Tyr
 530 535 540
 Phe Tyr Glu Glu Gly Glu Arg Glu
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